RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/073,138A_
Source: _/FW/6_
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RAW SEQUENCE LISTING   DATE: 08/31/2005
PATENT APPLICATION: US/10/073,138A   TIME: 16:57:51

Input Set : A:\US10073138.txt
Output Set: N:\CRF4\08312005\J073138A.raw

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 3 <110> APPLICANT: ANDERSON, DARRELL R.
 4        HANNA, NABIL
 5        BRAMS, PETER
 6        HEARD, CHERYL
 8 <120> TITLE OF INVENTION: INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
 9        CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
10        CO-STIMULATORY ANTIGENS
12 <130> FILE REFERENCE: 37003-280705
14 <140> CURRENT APPLICATION NUMBER: 10/073138A
15 <141> CURRENT FILING DATE: 2002-02-13
17 <150> PRIOR APPLICATION NUMBER: PCT/US97/19906
18 <151> PRIOR FILING DATE: 1997-10-29
20 <150> PRIOR APPLICATION NUMBER: 08/746,361
21 <151> PRIOR FILING DATE: 1996-11-08
23 <150> PRIOR APPLICATION NUMBER: 08/487,550
24 <151> PRIOR FILING DATE: 1995-06-07
26 <160> NUMBER OF SEQ ID NOS: 6
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
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33 <213> ORGANISM: Homo sapiens
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45 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
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49 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
50          35                  40                  45
52 aat gaa tat gtc cac tgg tac cag cag aag cca gcg cgg gcc cct ata  192
53 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
54      50                  55                  60
56 ctg gtc atc tat gat gat agt gac cgg ccc tca ggg atc cct gag cga  240
57 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
58  65                  70                  75                  80
60 ttc tct ggc tcc aaa tca ggg aac acc gcc acc ctg acc atc aac ggg  288
61 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
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68 gct agt gat cat ccg gtc ttc gga gga ggg acc cgg gtg acc gtc cta    384
69 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
70              115                 120                 125
72 ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct    432
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74       130                 135                 140
76 gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac    480
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78 145                 150                 155                 160
80 ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc    528
81 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
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84 gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac    576
85 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
86              180                 185                 190
88 aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag    624
89 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
90        195                 200                 205
92 tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg    672
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120 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
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123 agc ggt tac tac tac tgg acc tgg atc cgc cag acc cca ggg agg gga    192
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125        50                 55                  60
127 ctg gag tgg att ggc cat att tat ggt aat ggt gcg acc acc aac tac    240
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133                  85                  90                  95
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136 Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
137             100                 105                 110
139 gtc tat tac tgt gcg aga ggc cct cgc cct gat tgc aca acc att tgt    384
140 Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
141         115                 120                 125
143 tat ggc ggc tgg gtc gat gtc tgg ggc ccg gga gac ctg gtc acc gtc    432
144 Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
145     130                 135                 140
147 tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc    480
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149 145                 150                 155                 160
151 tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag    528
152 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
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155 gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg    576
156 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
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159 acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc    624
160 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
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165     210                 215                 220
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204 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
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248              20                  25                  30
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251 Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
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258 cca ggc caa cct cca agg ctc ctg att tat aag gtt tct aac cgg gac   240
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268                 100                 105                 110
270 tgc ggg caa ggt aca agg act cct ccc act ttc ggc gga ggg acc aag   384
271 Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys
272         115                 120                 125
274 gtg gaa atc aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg   432
275 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
276         130                 135                 140
278 cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg   480
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280 145                 150                 155                 160
282 ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat   528
283 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
284                 165                 170                 175
286 aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac   576
287 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
288                 180                 185                 190
290 agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa   624
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292         195                 200                 205
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295 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
296         210                 215                 220
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318 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
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